

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: January 7, 2002, 15:49:08 ; Search time 101.88 Seconds  
(without alignments)  
34.394 Million cell updates/sec

Title: US-08-569-749-7

Sequence: 1 LARAGFYITGPDRAVACFAC.....WEKPDAMSEHRRHPNCPF 46

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR68:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	269	100.0	618	2	S68450
2	256	95.2	618	2	JC5964
3	251	93.3	604	2	S68449
4	192	71.4	497	2	S69544
5	149	55.4	1232	2	A55478
6	140	52.0	496	2	S68452
7	140	52.0	497	2	S69545
8	138	51.3	1447	2	T42628
9	133.5	49.6	4845	2	T31067
10	132	49.1	268	2	T10304
11	132	49.1	268	2	A53989
12	127	47.2	298	3	JC7568
13	124	46.1	275	2	A45679
14	117	43.5	208	2	T03183
15	111	41.3	150	2	T28409
16	107	39.8	155	2	T30489
17	104	38.7	997	2	T43523
18	98	36.4	292	2	T41772
19	96	35.7	286	2	D36828
20	93	34.6	275	2	T10310
21	80	29.7	249	2	H72858
22	80	29.7	249	2	T41814
23	72	26.8	155	2	T37471
24	66.5	24.7	329	2	T28403
25	63.5	23.6	278	1	S25690
26	63	23.4	234	2	T30427
27	63	23.4	308	2	T37474
28	58.5	21.7	284	1	A41382
29	57	21.2	122	2	S09314

30	57	21.2	138	2	E48188	phospholipase A2 (
31	56.5	21.0	181	2	E36794	hypothetical prote
32	56	20.8	211	2	T15390	hypothetical prote
33	55	20.4	357	2	T50696	DNA primase small
34	55	20.4	409	2	S72438	phosphatidylserine
35	55	20.4	838	2	A48440	ring-infected eryt
36	54.5	20.3	424	2	E30857	hypothetical prote
37	54.5	20.3	424	2	T10400	alkaline exonuclea
38	54.5	20.3	517	1	D37831	phenol 2-monooxyge
39	54	20.1	355	2	C64549	conserved hypothet
40	54	20.1	355	2	G71958	hypothetical prote
41	54	20.1	954	2	S57108	hypothetical prote
42	54	20.1	1004	2	JH0470	Na+/K+-exchanging
43	53.5	19.9	297	2	T39905	protein transport
44	53.5	19.9	525	1	S39834	myd-related protei
45	53.5	19.9	5825	2	T12117	polyprotein - lava

## ALIGNMENTS

RESULT 1  
S68450  
apoptosis inhibitor hlap-2 - human  
C:Species: Homo sapiens (man)  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 21-Jul-2000  
C:Accession: S68450  
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha  
Nature 379, 349-353, 1996  
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of  
A:Reference number: A58182; MUID:96149249  
A:Accession: S68450  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-618 <LIS>  
A:Cross-references: EMBL:U45879; NID:q1184317; PIDN:AAC50372.1; PID:q1184318  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: RING finger homology  
C:Keywords: apoptosis; zinc finger  
F:567-611/Domain: RING finger homology <RING>

Query Match 100.0%, Score 269, DB 2, Length 618;  
Best Local Similarity 100.0%, Pred. No. 1.4e-25;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 LARAGFYITGPDRAVACFACGKLSNWEKPDAMSEHRRHPNCPF 46  
Db 204 LARAGFYITGPDRAVACFACGKLSNWEKPDAMSEHRRHPNCPF 249

RESULT 2  
JC5964  
apoptosis inhibitor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 02-Sep-2000  
C:Accession: JC5964  
R:Stehlik, C.; de Martin, R.; Binder, B.R.; Lippe, J.  
Biochem. Biophys. Res. Commun. 243, 827-832, 1998  
A:Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap)  
A:Reference number: JC5964; MUID:98162622  
A:Accession: JC5964  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-358 <STES>  
A:Cross-references: GB:U79142; NID:92957174; PIDN:AAC39171.1; PID:92957175  
C:Superfamily: RING finger homology  
F:307-351/Domain: RING finger homology <RRN>

Query Match 95.2%, Score 256, DB 2, Length 358;  
Best Local Similarity 93.5%, Pred. No. 3.4e-24;







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